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Pioneer Hi-Bred International, Inc.

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 Met Asp Met Glu Glu Lys Val Lys Arg Glu Ile Lys Ile Leu Arg Leu  
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 Gly His Phe Leu Lys Thr Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro  
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 50 55 60  
 Glu Ile Ser Val Met Lys Met Val Lys His Pro Asn Ile Val Glu Leu  
 65 70 75 80  
 His Glu Val Met Ala Ser Lys Ser Lys Ile Tyr Ile Ser Ile Glu Leu  
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 Val Arg Gly Gly Glu Leu Phe Asn Lys Val Ser Lys Gly Arg Leu Lys  
 100 105 110  
 Glu Asp Leu Ala Arg Leu Tyr Phe Gln Gln Leu Ile Ser Ala Val Asp  
 115 120 125  
 Phe Cys His Ser Arg Gly Val Tyr His Arg Asp Leu Lys Pro Glu Asn  
 130 135 140  
 Leu Leu Leu Asp Glu His Gly Asn Leu Lys Val Ser Asp Phe Gly Leu  
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 Thr Ala Phe Ser Asp His Leu Lys Glu Asp Gly Leu Leu His Thr Thr  
 165 170 175

Cys Gly Thr Pro Ala Tyr Val Ser Pro Glu Val Ile Ala Lys Lys Gly  
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 Tyr Asp Gly Ala Lys Ala Asp Ile Trp Ser Cys Gly Val Ile Leu Tyr  
 195 200 205  
 Val Leu Leu Ala Gly Phe Leu Pro Phe Gln Asp Asp Asn Leu Val Ala  
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 Met Tyr Lys Lys Ile His Arg Gly Asp Phe Lys Cys Pro Pro Trp Phe  
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 Ser Leu Asp Ala Arg Lys Leu Val Thr Lys Leu Leu Asp Pro Asn Pro  
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 Asn Thr Arg Ile Ser Ile Ser Lys Val Met Glu Ser Ser Trp Phe Lys  
 260 265 270  
 Lys Gln Val Pro Arg Lys Val Glu Glu Val Val Glu Lys Val Asp Leu  
 275 280 285  
 Glu Glu Lys Ile Glu Asn Gln Glu Thr Met Asn Ala Phe His Ile Ile  
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 Ser Leu Ser Glu Gly Phe Asn Leu Ser Pro Leu Phe Glu Glu Lys Arg  
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 Ser Glu Thr Lys Val Arg Leu Gln Gly Gln Glu Arg Gly Arg Lys Gly  
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 Lys Leu Ala Ile Ala Ala Asp Ile Tyr Ala Val Thr Pro Ser Phe Met  
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 Val Val Glu Val Lys Lys Asp Asn Gly Asp Thr Leu Glu Tyr Asn Gln  
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 <213> Glycine max

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 Val Lys Ile Ala Glu His Val Leu Thr Gly His Lys Val Ala Ile Lys  
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 Ile Leu Asn Arg Arg Lys Ile Lys Asn Met Glu Met Glu Glu Lys Val  
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 Arg Arg Glu Ile Lys Ile Leu Arg Leu Phe Met His Pro His Ile Ile  
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 Arg Leu Tyr Glu Val Ile Glu Thr Pro Thr Asp Ile Tyr Val Val Met  
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 Glu Tyr Val Lys Ser Gly Glu Leu Phe Asp Tyr Ile Val Glu Lys Gly  
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 Arg Leu Gln Glu Asp Glu Ala Arg Asn Phe Phe Gln Gln Ile Ile Ser  
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Gly Val Glu Tyr Cys His Arg Asn Met Val Val His Arg Asp Leu Lys  
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 Pro Glu Asn Leu Leu Leu Asp Ser Lys Cys Asn Val Lys Ile Ala Asp  
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 Phe Gly Leu Ser Asn Ile Met Arg Asp Gly His Phe Leu Lys Thr Ser  
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 Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser Gly Lys Leu  
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 Tyr Ala Gly Pro Glu Val Asp Val Trp Ser Cys Gly Val Ile Leu Tyr  
 195 200 205  
 Ala Leu Leu Cys Gly Thr Leu Pro Phe Asp Asp Glu Asn Ile Pro Asn  
 210 215 220  
 Leu Phe Lys Lys Ile Lys Gly Gly Ile Tyr Thr Leu Pro Ser His Leu  
 225 230 235 240  
 Ser Pro Gly Ala Arg Asp Leu Ile Pro Gly Met Leu Val Val Asp Pro  
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 Met Arg Arg Met Thr Ile Pro Glu Ile Arg Gln His Pro Trp Phe Gln  
 260 265 270  
 Ala Arg Leu Pro Arg Tyr Leu Ala Val Pro Pro Pro Asp Thr Met Gln  
 275 280 285  
 Gln Ala Lys Lys Ile Asp Glu Glu Ile Leu Gln Glu Val Val Lys Met  
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 Gly Phe Asp Arg Asn Gln Leu Val Glu Ser Leu Gly Asn Arg Ile Gln  
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 Asn Glu Gly Thr Val Ala Tyr Tyr Leu Leu Leu Asp Asn Arg Phe Arg  
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 Val Ser Ser Gly Tyr Leu Gly Ala Glu Phe Gln Glu Thr Met Asp Ser  
 340 345 350  
 Gly Phe Asn Gln Met His Ser Ser Glu Leu Ala Ser Ser Val Val Gly  
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 Asn Arg Phe Pro Gly Tyr Met Glu Tyr Pro Gly Val Gly Ser Arg Gln  
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 Asn Val Cys Trp Lys Lys Ile Gly His Tyr Asn Met Lys Cys Arg Trp  
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 Val Ala Gly Ile Pro Gly His His Glu Gly Met Val Asn Asn Asn Val  
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His Ser Asn His Tyr Phe Gly Asp Asp Ser Asn Ile Ile Glu Asn Asp  
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Ala Val Ser Thr Ser Asn Val Val Lys Phe Glu Val Gln Leu Tyr Lys  
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Thr Arg Glu Glu Lys Tyr Leu Leu Asp Leu Gln Arg Val Gln Gly Pro  
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Ala Lys Val Tyr His Ala Arg His Leu Lys Thr Gly Lys Ser Val Ala  
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Met Lys Val Val Gly Lys Glu Lys Val Val Lys Val Gly Met Met Glu  
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Gln Ile Lys Arg Glu Ile Ser Ala Met Asn Met Val Lys His Pro Asn  
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Ile Val Gln Leu His Glu Val Met Ala Ser Lys Ser Lys Ile Tyr Ile  
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Ala Met Glu Leu Val Arg Gly Gly Glu Leu Phe Asn Lys Ile Ala Arg  
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Gly Arg Leu Arg Glu Glu Met Ala Arg Leu Tyr Phe Gln Gln Leu Ile  
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Ser Ala Val Asp Phe Cys His Ser Arg Gly Val Tyr His Arg Asp Leu  
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Lys Pro Glu Asn Leu Leu Leu Asp Asp Asp Gly Asn Leu Lys Val Thr  
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Asp Phe Gly Leu Ser Thr Phe Ser Glu His Leu Arg His Asp Gly Leu  
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Leu His Thr Thr Cys Gly Thr Pro Ala Tyr Val Ala Pro Glu Val Ile  
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Gly Lys Arg Gly Tyr Asp Gly Ala Lys Ala Asp Ile Trp Ser Cys Gly  
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Val Ile Leu Tyr Val Leu Leu Ala Gly Phe Leu Pro Phe Gln Asp Asp  
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Asn Leu Val Ala Leu Tyr Lys Lys Ile Tyr Arg Gly Asp Phe Lys Cys  
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Pro Pro Trp Phe Ser Ser Glu Ala Arg Arg Leu Ile Thr Lys Leu Leu  
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Asp Pro Asn Pro Asn Thr Arg Ile Thr Ile Ser Lys Ile Met Asp Ser  
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Ser Trp Phe Lys Lys Pro Val Pro Lys Asn Leu Met Gly Lys Lys Arg  
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Glu Glu Leu Asp Leu Glu Glu Lys Ile Lys Gln His Glu Gln Glu Val  
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Ser Thr Thr Met Asn Ala Phe His Ile Ile Ser Leu Ser Glu Gly Phe  
305 310 315 320

Asp Leu Ser Pro Leu Phe Glu Glu Lys Lys Arg Glu Glu Lys Glu Leu  
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Arg Phe Ala Thr Thr Arg Pro Ala Ser Ser Val Ile Ser Arg Leu Glu  
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Val Arg Leu Gln Gly Gln Glu Lys Gly Arg Lys Gly Lys Leu Ala Ile  
370 375 380

Ala Ala Asp Leu Tyr Ala Val Thr Pro Ser Phe Leu Val Val Glu Val  
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Lys Lys Asp Asn Gly Asp Thr Leu Glu Tyr Asn Gln Phe Cys Ser Lys  
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Glu Asn Pro Thr Leu Ala  
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 Lys Ile Leu Asn Arg His Lys Ile Lys Asn Met Glu Met Glu Glu Lys  
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 Val Arg Arg Glu Ile Lys Ile Leu Arg Leu Phe Met His His His Ile  
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 Ile Arg Leu Tyr Glu Val Val Glu Thr Pro Thr Asp Ile Tyr Val Val  
 85 90 95  
 Met Glu Tyr Val Lys Ser Gly Glu Leu Phe Asp Tyr Ile Val Glu Lys  
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 Gly Arg Leu Gln Glu Asp Glu Ala Arg His Phe Phe Gln Gln Ile Ile  
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 Ser Gly Val Glu Tyr Cys His Arg Asn Met Val Val His Arg Asp Leu  
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 Lys Pro Glu Asn Leu Leu Leu Asp Ser Lys Phe Asn Ile Lys Ile Ala  
 145 150 155 160  
 Asp Phe Gly Leu Ser Asn Ile Met Arg Asp Gly His Phe Leu Lys Thr  
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Leu Tyr Ala Gly Pro Glu Val Asp Val Trp Ser Cys Gly Val Ile Leu  
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 Tyr Ala Leu Leu Cys Gly Thr Leu Pro Phe Asp Asp Glu Asn Ile Pro  
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 Asn Leu Phe Lys Lys Ile Lys Gly Gly Ile Tyr Thr Leu Pro Ser His  
 225 230 235 240  
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 245 250 255  
 Pro Met Lys Arg Met Thr Ile Pro Glu Ile Arg Gln His Pro Trp Phe  
 260 265 270  
 Gln Val His Leu Pro Arg Tyr Leu Ala Val Pro Pro Pro Asp Thr Leu  
 275 280 285  
 Gln Gln Ala Lys Lys Ile Asp Glu Glu Ile Leu Gln Glu Val Val Asn  
 290 295 300  
 Met Gly Phe Asp Arg Asn Gln Leu Val Glu Ser Leu Ser Asn Arg Ile  
 305 310 315 320  
 Gln Asn Glu Gly Thr Val Thr Tyr Tyr Leu Leu Leu Asp Asn Arg Phe  
 325 330 335  
 Arg Val Ser Ser Gly Tyr Leu Gly Ala Glu Phe Gln Glu Thr Met Asp  
 340 345 350  
 Ser Gly Phe Asn Arg Met His Ser Gly Glu Val Ala Ser Pro Val Val  
 355 360 365  
 Gly His His Ser Thr Gly Tyr Met Asp Tyr Gln Gly Val Gly Met Arg  
 370 375 380  
 Gln Gln Phe Pro Val Glu Arg Lys Trp Ala Leu Gly Leu Gln Ser Arg  
 385 390 395 400  
 Ala Gln Pro Arg Glu Ile Met Thr Glu Val Leu Lys Ala Leu Gln Glu  
 405 410 415  
 Leu Asn Val Cys Trp Lys Lys Ile Gly His Tyr Asn Met Lys Cys Arg  
 420 425 430  
 Trp Val Ala Gly Thr Ala Gly His His Glu Gly Met Ile Asn Asn Ser  
 435 440 445  
 Leu His Ser Asn His Tyr Phe Gly Asn Asp Ser Gly Ile Ile Glu Asn  
 450 455 460  
 Glu Ala Val Ser Lys Ser Asn Val Val Lys Phe Glu Val Gln Leu Tyr  
 465 470 475 480  
 Lys Thr Arg Glu Glu Lys Tyr Leu Leu Asp Leu Gln Arg Val Gln Gly  
 485 490 495  
 Pro Gln Phe Leu Phe Leu Asp Leu Cys Ala Ala Phe Leu Ser Gln Leu  
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Arg Val Leu  
515

<210> 17  
<211> 1869  
<212> DNA  
<213> Glycine max

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tgctcgggtc cactgcagaa tttcagttta ttcttatcta gctcaattct gggtgtgggt 180  
ttatctctta ctggaagaca gactttgagg tagactcctt ataagtgcgc agaagttcaa 240  
gtgtagagaa tgagtcagcc taagattaaa cgcgaggttg gtaaatacga ggtggggagg 300  
accattggtg aaggtacatt tgcaaagggt aaatttgcaa ggaactctga gacaggagag 360  
cccgtggctc ttaaaattct tgacaaggag aaggtgctaa agcacaagat ggctgagcag 420  
atcaggagag aagtagctac aatgaaacta atcaagcatc caaatgttgt tcgattgtat 480  
gaggtcatgg gaagcaagac caaaatatat attgtttgg agtttgaac tgggggggaa 540  
ctctttgaca aaattgtaaa ccatggaagg atgagtgaaa atgaagcacg tagatatttc 600  
cagcagctta taaatgctgt tgattattgc catagcaggg gtgtctacca cagagacctg 660  
aagccagaaa atttgctatt agatacttat gggaacctta aagtttctga ttttggtttg 720  
agtgcctctc ccagcaagt tagggatgat ggacttcttc atactacatg tggcactcca 780  
aattatgttg ctctgaggt ccttaacgat agaggctatg atggggcaac tgcagacttg 840  
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actatacctg agattttgga tgatgaatgg ttttaagaaag aatataagcc tccattttt 1080  
gaggagaatg gggaaatcaa cctcgatgat gttgaagctg tctttaaaga ctctgaagag 1140  
caccatgtga cagagaaaaa agaagagcag cctacagcca tgaatgcatt tgagttaatc 1200  
tccatgtcca aaggactgaa ccttgaaaac ttgtttgata ctgagcaggg atttaaaagg 1260  
gaaacaagat tcaactcaaa atcccctgcg gatgagataa tcaacaagat tgaggaagcc 1320  
gcaaaacctc ttggctttga tgtgcagaag aaaaattaca agatgaggct tgcaaatgtg 1380  
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aagaaacttt caacaagcct ggatgatgtt gtttggaaaa cagaagatga tatgcaaatg 1560  
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aaaaaaaaa 1869

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<211> 441  
<212> PRT  
<213> Glycine max

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Ser Glu Thr Gly Glu Pro Val Ala Leu Lys Ile Leu Asp Lys Glu Lys  
35 40 45  
Val Leu Lys His Lys Met Ala Glu Gln Ile Arg Arg Glu Val Ala Thr  
50 55 60

Met Lys Leu Ile Lys His Pro Asn Val Val Arg Leu Tyr Glu Val Met 80  
 65 70 75  
 Gly Ser Lys Thr Lys Ile Tyr Ile Val Leu Glu Phe Val Thr Gly Gly 95  
 85 90  
 Glu Leu Phe Asp Lys Ile Val Asn His Gly Arg Met Ser Glu Asn Glu 110  
 100 105  
 Ala Arg Arg Tyr Phe Gln Gln Leu Ile Asn Ala Val Asp Tyr Cys His 125  
 115 120  
 Ser Arg Gly Val Tyr His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu 140  
 130 135  
 Asp Thr Tyr Gly Asn Leu Lys Val Ser Asp Phe Gly Leu Ser Ala Leu 160  
 145 150 155  
 Ser Gln Gln Val Arg Asp Asp Gly Leu Leu His Thr Thr Cys Gly Thr 175  
 165 170  
 Pro Asn Tyr Val Ala Pro Glu Val Leu Asn Asp Arg Gly Tyr Asp Gly 190  
 180 185  
 Ala Thr Ala Asp Leu Trp Ser Cys Gly Val Ile Leu Phe Val Leu Val 205  
 195 200  
 Ala Gly Tyr Leu Pro Phe Asp Asp Pro Asn Leu Met Asn Leu Tyr Lys 220  
 210 215  
 Lys Ile Ser Ala Ala Glu Phe Thr Cys Pro Pro Trp Leu Ser Phe Thr 240  
 225 230 235  
 Ala Arg Lys Leu Ile Thr Arg Ile Leu Asp Pro Asp Pro Thr Thr Arg 255  
 245 250  
 Ile Thr Ile Pro Glu Ile Leu Asp Asp Glu Trp Phe Lys Lys Glu Tyr 270  
 260 265  
 Lys Pro Pro Ile Phe Glu Glu Asn Gly Glu Ile Asn Leu Asp Asp Val 285  
 275 280  
 Glu Ala Val Phe Lys Asp Ser Glu Glu His His Val Thr Glu Lys Lys 300  
 290 295  
 Glu Glu Gln Pro Thr Ala Met Asn Ala Phe Glu Leu Ile Ser Met Ser 320  
 305 310 315  
 Lys Gly Leu Asn Leu Glu Asn Leu Phe Asp Thr Glu Gln Gly Phe Lys 335  
 325 330  
 Arg Glu Thr Arg Phe Thr Ser Lys Ser Pro Ala Asp Glu Ile Ile Asn 350  
 340 345  
 Lys Ile Glu Glu Ala Ala Lys Pro Leu Gly Phe Asp Val Gln Lys Lys 365  
 355 360  
 Asn Tyr Lys Met Arg Leu Ala Asn Val Lys Ala Gly Arg Lys Gly Asn 380  
 370 375

Leu Asn Val Ala Thr Glu Ile Phe Gln Val Ala Pro Ser Leu His Met  
385 390 395 400

Val Glu Val Arg Lys Ala Lys Gly Asp Thr Leu Glu Phe His Lys Phe  
405 410 415

Tyr Lys Lys Leu Ser Thr Ser Leu Asp Asp Val Val Trp Lys Thr Glu  
420 425 430

Asp Asp Met Gln Met Arg Glu Thr Lys  
435 440

<210> 19  
<211> 817  
<212> DNA  
<213> Triticum aestivum

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gaacattagg tataggcaca tttggaaaag tgaggattgc agagcataag catacagggc 180  
ataaagttgc tataaagatt ctgaaccgtc gtcaaataag aactatggaa atggaggaga 240  
aagcaaagag agagatcaag atattgaggt tgttcatcca cctcatatc atccggcttt 300  
atgaggtcat ttacacacct acagatatat ttgttgtgat ggaatattgc aagtatgggt 360  
agctattcga ctgcattggt gagaaagggc ggttacagga agatgaggct cgtcgaatct 420  
tccagcagat tatatctggt gttgaatact gccacagaaa catggttgct catcgtgatc 480  
taaagccaga gaacctgtta cttgattcca aatacaatgt gaaacttgcc gactttgggt 540  
taagtaatgt catgcatgat ggccattttc tgaagactag ctgcgggagt ccaaactatg 600  
ctgcaccaga gggtatctca ggtaaattat acgctggacc tgagggtgat gtttggagct 660  
gcgggggtgat actttatgct cttctttgtg gcactcttcc atttgatgat gacaatatc 720  
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ctgcaaggga ttgatccaag aatgcttggt gttgatc 817

<210> 20  
<211> 244  
<212> PRT  
<213> Triticum aestivum

<400> 20  
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Tyr Asn Val Gly Arg Thr Leu Gly Ile Gly Thr Phe Gly Lys Val Arg  
20 25 30

Ile Ala Glu His Lys His Thr Gly His Lys Val Ala Ile Lys Ile Leu  
35 40 45

Asn Arg Arg Gln Met Arg Thr Met Glu Met Glu Glu Lys Ala Lys Arg  
50 55 60

Glu Ile Lys Ile Leu Arg Leu Phe Ile His Pro His Ile Ile Arg Leu  
65 70 75 80

Tyr Glu Val Ile Tyr Thr Pro Thr Asp Ile Phe Val Val Met Glu Tyr  
85 90 95

Cys Lys Tyr Gly Glu Leu Phe Asp Cys Ile Val Glu Lys Gly Arg Leu  
100 105 110

Gln Glu Asp Glu Ala Arg Arg Ile Phe Gln Gln Ile Ile Ser Gly Val  
115 120 125

Glu Tyr Cys His Arg Asn Met Val Ala His Arg Asp Leu Lys Pro Glu  
130 135 140

Asn Leu Leu Leu Asp Ser Lys Tyr Asn Val Lys Leu Ala Asp Phe Gly  
145 150 155 160

Leu Ser Asn Val Met His Asp Gly His Phe Leu Lys Thr Ser Cys Gly  
165 170 175

Ser Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser Gly Lys Leu Tyr Ala  
180 185 190

Gly Pro Glu Val Asp Val Trp Ser Cys Gly Val Ile Leu Tyr Ala Leu  
195 200 205

Leu Cys Gly Thr Leu Pro Phe Asp Asp Asp Asn Ile Pro Lys Leu Phe  
210 215 220

Lys Lys Ile Lys Gly Gly Ile Tyr Ile Leu Pro Ser His Leu Ser Ala  
225 230 235 240

Pro Ala Arg Asp

<210> 21

<211> 2006

<212> DNA

<213> Triticum aestivum

<400> 21

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tggggattgg	ttcgttcggg	aaggtcaaga	tgcccgagca	tataaaaaact	ggtcacaagg	180
tggccgtcaa	gacccctaac	cgccggaaaa	tcaaaaacat	ggagatggaa	gagaaagtga	240
aaagagagat	caagatatta	agattattca	tgcacccaca	tatcatccgc	ctttatgaag	300
tgatagaggc	accagctgat	atztatgtgg	ttatggagta	tgtaagtct	ggtgaattgt	360
ttgattacat	tggtgagaaa	ggtaggctac	aggaggaaga	ggcccgccgt	ttctttcaac	420
agatcatatc	tggtgttcaa	tattgccaca	ggaacatggt	ggtgcaccgc	gatctaaagc	480
cggagaacct	tcttttgac	aataattgtg	atgttaagat	tgccgatttt	ggcttaagta	540
atgttatgcg	tgacggccac	tttcttaaga	caagttgtgg	tagcccaaact	tatgcagctc	600
cggagggttat	atctggaaaa	ctgtacgctg	ggcctgaagt	tgatgtatgg	agctgcggtg	660
ttattcttta	tgctcttcta	tgtggtactc	ttccatttga	tgatgagaac	ataccaacc	720
tttttaagaa	aataaagggt	ggaatatata	cccttccaag	ccatttatca	ggcccagcaa	780
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tacgcgagca	tccatggttt	gaagctcaac	tcccacgata	tttagccgtg	cctccaccag	900
atactgcaca	acaagttaaa	aagattgatg	aagaatctct	tgtaaaagt	atcagtctgg	960
gatttgacaa	aaacctgctg	gttgaatcaa	ttcataatag	attgcaaaat	gaggcaacag	1020
ttgcatatta	tttgtttttg	gataataaga	gtcgacaaac	aactggctat	cttggagctg	1080
ggtatcaaga	agctatggaa	tcgtctttct	caccatttac	tccaagtga	acacaaagtc	1140
cagctcatgg	aaatcgga	caaccatata	tggaatctcc	agttggcttg	agaccacatt	1200
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tgactgaagt	gctgaaggct	ctgcaagaac	tgaatgtata	ctggaaaaaa	attggacact	1320
ataacatgaa	atgtagatgg	agtcctcctg	gctttcccgg	tcaggagaat	atgaatcata	1380
ccaattataa	cttcagtga	gagcctattg	aaaccgacga	cctgggtgac	aagttaaatt	1440
taattaagtt	cgaacttcag	ctttacaaaa	caagagatga	gaaatacctt	ctggatttgc	1500
aaagggcgag	cgggcccgc	ctcctctttc	ttgatctatg	tgccgccttt	ctagctcagc	1560
tgagagtcct	ttgataccag	atgtgcccca	ggaatgtatg	ttgtatcact	ctaaagagat	1620

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gtaaatagca agctttctcc agcggatcaa agtcgtggag tatgtagaca tgcggagctg 1680
ttgtgtgctt atttcggcgc ctatatgctg aatttagacc tggcaggggc gggcaagtga 1740
agcaagcaag gaactattgc catcagggtta ttccagctg ccgccaagg cactaggata 1800
tagaagtatt actgattaat cctatatggg ccccttgga catactccta ctctactgct 1860
gtttacttgc atgtaatttt tactgtctgg gtctccagac cagaccacgt acacgaataa 1920
tttcttcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
aaaaaaaaaa aaaaaaaaaa aaaaaa

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<210> 22  
 <211> 523  
 <212> PRT  
 <213> Triticum aestivum

<400> 22

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Ala Arg Trp Lys Met Glu Thr Gly Gly Lys Asp Gly Asn Pro Leu Lys  
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Asn Tyr Arg Ile Gly Lys Thr Leu Gly Ile Gly Ser Phe Gly Lys Val  
 35 40 45

Lys Ile Ala Glu His Ile Lys Thr Gly His Lys Val Ala Val Lys Ile  
 50 55 60

Leu Asn Arg Arg Lys Ile Lys Asn Met Glu Met Glu Glu Lys Val Lys  
 65 70 75 80

Arg Glu Ile Lys Ile Leu Arg Leu Phe Met His Pro His Ile Ile Arg  
 85 90 95

Leu Tyr Glu Val Ile Glu Ala Pro Ala Asp Ile Tyr Val Val Met Glu  
 100 105 110

Tyr Val Lys Ser Gly Glu Leu Phe Asp Tyr Ile Val Glu Lys Gly Arg  
 115 120 125

Leu Gln Glu Glu Glu Ala Arg Arg Phe Phe Gln Gln Ile Ile Ser Gly  
 130 135 140

Val Gln Tyr Cys His Arg Asn Met Val Val His Arg Asp Leu Lys Pro  
 145 150 155 160

Glu Asn Leu Leu Leu Asp Asn Asn Cys Asp Val Lys Ile Ala Asp Phe  
 165 170 175

Gly Leu Ser Asn Val Met Arg Asp Gly His Phe Leu Lys Thr Ser Cys  
 180 185 190

Gly Ser Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser Gly Lys Leu Tyr  
 195 200 205

Ala Gly Pro Glu Val Asp Val Trp Ser Cys Gly Val Ile Leu Tyr Ala  
 210 215 220

Leu Leu Cys Gly Thr Leu Pro Phe Asp Asp Glu Asn Ile Pro Asn Leu  
 225 230 235 240

Phe Lys Lys Ile Lys Gly Gly Ile Tyr Thr Leu Pro Ser His Leu Ser  
 245 250 255  
 Gly Pro Ala Arg Asp Leu Ile Pro Arg Met Leu Val Val Asp Pro M t  
 260 265 270  
 Lys Arg Ile Thr Ile Arg Glu Ile Arg Glu His Pro Trp Phe Glu Ala  
 275 280 285  
 Gln Leu Pro Arg Tyr Leu Ala Val Pro Pro Pro Asp Thr Ala Gln Gln  
 290 295 300  
 Val Lys Lys Ile Asp Glu Glu Ser Leu Val Lys Val Ile Ser Leu Gly  
 305 310 315 320  
 Phe Asp Lys Asn Leu Leu Val Glu Ser Ile His Asn Arg Leu Gln Asn  
 325 330 335  
 Glu Ala Thr Val Ala Tyr Tyr Leu Phe Leu Asp Asn Lys Ser Arg Thr  
 340 345 350  
 Thr Thr Gly Tyr Leu Gly Ala Gly Tyr Gln Glu Ala Met Glu Ser Ser  
 355 360 365  
 Phe Ser Pro Ile Thr Pro Ser Glu Thr Gln Ser Pro Ala His Gly Asn  
 370 375 380  
 Arg Gln Gln Pro Tyr Met Glu Ser Pro Val Gly Leu Arg Pro His Phe  
 385 390 395 400  
 Pro Ala Asp Arg Lys Trp Ala Leu Gly Leu Gln Ser Arg Ala His Pro  
 405 410 415  
 Arg Glu Val Met Thr Glu Val Leu Lys Ala Leu Gln Glu Leu Asn Val  
 420 425 430  
 Tyr Trp Lys Lys Ile Gly His Tyr Asn Met Lys Cys Arg Trp Ser Pro  
 435 440 445  
 Pro Gly Phe Pro Gly Gln Glu Asn Met Asn His Thr Asn Tyr Asn Phe  
 450 455 460  
 Ser Ala Glu Pro Ile Glu Thr Asp Asp Leu Gly Asp Lys Leu Asn Leu  
 465 470 475 480  
 Ile Lys Phe Glu Leu Gln Leu Tyr Lys Thr Arg Asp Glu Lys Tyr Leu  
 485 490 495  
 Leu Asp Leu Gln Arg Ala Ser Gly Pro His Leu Leu Phe Leu Asp Leu  
 500 505 510  
 Cys Ala Ala Phe Leu Ala Gln Leu Arg Val Phe  
 515 520

<210> 23  
 <211> 512  
 <212> DNA  
 <213> Zea mays



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<400> 23  
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 catagaggga ggaggcgcg cggagatggt gggcggtggc ggccggcggc cgctgcggcg 120  
 ggtgggcâag tacgaggtgg gacgcacat cggggaaggc accttcgcca aggtcaagtt 180  
 cgcgcagaac accgagaccg gggagagcgt cgccatgaag gtgctcgacc gtcctccat 240  
 cctcaagaac aagatggccg aacagattaa gagagaaata tccataatga agcttgtag 300  
 gcatcccaat gtcgttaggc tacacgaggt ttggcgaagc cggaagaaga tatttataat 360  
 tctggagttc atcactggcg gcgagctatt cgataaaatt attcgtcatg ggagactcag 420  
 tgaagcagat gcccgagat actttcagca gcttattgat ggtgttgatt tttgtcacia 480  
 gaaaggagtc taccatcgag acttaaagcc tg 512

<210> 24  
 <211> 132  
 <212> PRT  
 <213> Zea mays

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 Phe Ala Lys Val Lys Phe Ala Gln Asn Thr Glu Thr Gly Glu Ser Val 30  
 20 25 30  
 Ala Met Lys Val Leu Asp Arg Ser Ser Ile Leu Lys Asn Lys Met Ala 45  
 35 40 45  
 Glu Gln Ile Lys Arg Glu Ile Ser Ile Met Lys Leu Val Arg His Pro 60  
 50 55 60  
 Asn Val Val Arg Leu His Glu Val Leu Ala Ser Arg Lys Lys Ile Phe 80  
 65 70 75 80  
 Ile Ile Leu Glu Phe Ile Thr Gly Gly Glu Leu Phe Asp Lys Ile Ile 95  
 85 90 95  
 Arg His Gly Arg Leu Ser Glu Ala Asp Ala Arg Arg Tyr Phe Gln Gln 110  
 100 105 110  
 Leu Ile Asp Gly Val Asp Phe Cys His Lys Lys Gly Val Tyr His Arg 125  
 115 120 125  
 Asp Leu Lys Pro 130

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 <211> 552  
 <212> DNA  
 <213> Glycine max

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 <221> unsure  
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 ttccactgca gaatttcagt ttattcttat ctagctcaat tctggttggg ggtttatctc 180  
 ttactggaag acagactttg aggtagactc cttataagtg cgcagaagtt caagtgtaga 240  
 gaatgagtca gcctaagatt aaacgccgag ttggtaaata cgaggtgggg aggaccattg 300  
 gtgaaggtag atttgcaaag gtgaaatttg caaggaactc tgagacagga gagccgtggc 360

tctttaaatt cttgacaagg agaangtgct aaagcacaag atggctgagc agatcaggag 420  
 agaagtagct acaatgaaac taatcaagca tccaaatgtt gttcgattgt atgaagtcac 480  
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 gtaaccatgg aa 552

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 <211> 77  
 <212> PRT  
 <213> Glycine max

<220>  
 <221> UNSURE  
 <222> (39)

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 Lys Val Lys Phe Ala Arg Asn Ser Glu Thr Gly Glu Pro Trp Leu Leu  
                   20                  25                  30  
 Lys Phe Leu Thr Arg Arg Xaa Val Leu Lys His Lys Met Ala Glu Gln  
           35                  40                  45  
 Ile Arg Arg Glu Val Ala Thr Met Lys Leu Ile Lys His Pro Asn Val  
           50                  55                  60  
 Val Arg Leu Tyr Glu Val Met Gly Ser Lys Thr Asn Ile  
           65                  70                  75

<210> 27  
 <211> 391  
 <212> DNA  
 <213> Triticum aestivum

<220>  
 <221> unsure  
 <222> (179)

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WO 00/36115

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 tggggattgg ttcggttcggg aagggtcaaga ttgccgagca tataaaaact ggtcacaang 180  
 tgcccggtcaa gacccctaac cgccggcaaa tcaaaaacat ggcgatggaa gagaangtgn 240  
 caagagagat caagatatta agattattca tgcacccaca tatcatccgc ctttatnaag 300  
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 nttgattata ntgtttctaa ngctctntata t 391

<210> 28  
 <211> 85  
 <212> PRT  
 <213> Triticum aestivum

<220>  
 <221> UNSURE  
 <222> (29)

<220>  
 <221> UNSURE  
 <222> (48)

<220>  
 <221> UNSURE  
 <222> (50)

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&lt;221&gt; UNSURE

&lt;222&gt; (69)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (75)

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&lt;222&gt; (80)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (82)

&lt;400&gt; 28

Leu Lys Asn Tyr Arg Ile Gly Lys Thr Leu Gly Ile Gly Ser Phe Gly  
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Lys Val Lys Ile Ala Glu His Ile Lys Thr Gly His Xaa Val Ala Val  
 20 25 30

Lys Ile Leu Asn Arg Arg Gln Ile Lys Asn Met Ala Met Glu Glu Xaa  
 35 40 45

Val Xaa Arg Glu Ile Lys Ile Leu Arg Leu Phe Met His Pro His Ile  
 50 55 60

Ile Arg Leu Tyr Xaa Val Ile Glu Ala Pro Xaa Asp Ile Tyr Val Xaa  
 65 70 75 80

Met Xaa Tyr Val Lys  
 85